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FIG. 1A-1

1	GTCGACCCAC GCGTCCGAGA AGAAACCCT AGATTCTCC GTCTCTCTAA TTTCTTTCT	
61	CTCTCAAGCT TCTCAGAAAG TCTGACACTT TCGAGAATCT AATCTCCAA TTTCTTGCT	
121	TTTTGGAGAA GGAATCGAAT T ATG TAC AAG GAA CGT AGT GGA GGA GGT GGT GGT TCA Met Tyr Lys Lys Glu Arg Ser Gly Gly Gly Gly Ser	13
181	TCG AGA TCA GAG ATC CTC GGT GGA GCT ATT GAT CGG AAA CGA ATC AAC GAT GCA CTC AAT Ser Arg Ser Glu Ile Leu Gly Gly Ala Ile Asp Arg Lys Arg Ile Asn Asp Ala Leu Asn	33
241	AAG AAA CTA GAG AAA TCT TCA ACT TCC ACC ACC ACA TCT AGG GTT TTC TCT TCT AAA GAC Lys Lys Leu Glu Lys Ser Ser Thr Thr Thr Ser Arg Val Phe Ser Ser Lys Asp	53
301	AAA GAT CCC TTT TCC TCA TCT ACT AAA ACT CAG CTT CCT GAT GTG GAA TCG GAA ACT Lys Asp Pro Phe Ser Phe Thr Ser Thr Lys Thr Gln Leu Pro Asp Val Glu Ser Glu Thr	73
361	GAT AGT GAA GGG TCT GAT GTG AGT GGA TCG GAG GGT GAT GAT ACG TCG TGG ATC TCT TGG Asp Ser Glu Gly Ser Asp Val Ser Gly Ser Glu Gly Asp Thr Ser Trp Ile Ser Trp	93
421	TTT TGT AAT TTG AGA GGG AAT GAT TTC TTC TGT GAA GTC GAT GAA GAT TAT ATT CAA GAT Phe Cys Asn Leu Arg Gly Asn Asp Phe Phe Cys Glu Val Asp Glu Asp Tyr Ile Gln Asp	113
481	GAT TTC AAT CTT TGT GGT TTA AGT GGT CAA GTC CCT TAC TAT GAT TAT GCA CTT GAT CTC Asp Phe Asn Leu Cys Gly Leu Ser Gly Gln Val Pro Tyr Tyr Asp Tyr Ala Leu Asp Leu	133
541	ATT TTA GAT GTT GAT GCT TCC AAC AGT GAG ATG TTT ACT GAT GAA CAG CAT GAA ATG GTG Ile Leu Asp Val Asp Ala Ser Asn Ser Glu Met Phe Thr Asp Glu Gln His Glu Met Val	153



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FIG. 1A-2

601	GAA TCA GCT GCT GAG ATG CTA TAT GGT CTT ATT CAT GTT TAC ATT TTG ACT ACT AAA Glu Ser Ala Ala Ala Glu Met Tyr Gly Leu Ile His Val Arg Tyr Ile Leu Thr Thr Lys	173
661	GGA ATG GCT GCA ATG ACT GAG AAG TAC AAG AAC TGT GAT TTC GGG AGA TGC CCG AGA GTT Gly Met Ala Ala Met Thr Glu Lys Tyr Lys Asn Cys Asp Phe Gly Arg Cys Pro Arg Val	193
721	TTC TGT TGC GGT CAG TCT TGT CTT CCA GTT GGA CAA TCC GAT ATC CCG AGA TCG AGT ACT Phe Cys Cys Gly Gln Ser Cys Leu Pro Val Gly Gln Ser Asp Ile Pro Arg Ser Ser Thr	213
781	GTG AAG ATA TAC TGC CCT AAA TGC GAG GAT ATA TCT TAC CCG CGA TCT AAA TTC CAA GGC Val Lys Ile Tyr Cys Pro Lys Cys Glu Asp Ile Ser Tyr Pro Arg Ser Lys Phe Gln Gly	233
841	AAT ATT GAT GGA GCG TAC TTT GGA ACC ACA TTC CCT CAC TTG TTC TTG ATG ACT TAC GGG Asn Ile Asp Gly Ala Tyr Phe Gly Thr Thr Phe Pro His Leu Phe Leu Met Thr Tyr Gly	253
901	AAC TTA AAG CCG CAG AAG CCT ACT CAA AGC TAT GTC CCA AAA ATC TTT GGC TTC AAG GTA Asn Leu Lys Pro Gln Lys Pro Thr Gln Ser Tyr Val Pro Lys Ile Phe Gly Phe Lys Val	273
960	CAC AAA CCA TGATACTAGT GCTCTGCATT CTCATGGTG ATACATTTAG TGGCTCTGTA His Lys Pro	276
1020	ATTGCATCCG GATGAGCAAC TGAACAGGATA GCTGCGGTGA CTGGAGCATA CATCAACCAT T	

CKB1	MYRDR....GTVNSRPEV....VDRKRIND.....ALER.....PS	28
	: : : : : .	
CKB3	MYKERSGGGGGSSSRSEILGGAIDRK RIND.....ALNKKLEKSSTS	42
	: . . : : : : : : : . .	
CKB2	MYRER....GMVGSKSEV....VDRKRINEIHDNRPSHSMSQP VNGKGKV	42
CKB1	PSTSRQVNGK...GKGTVTAAT.TTANLIGKQQSNNINHRDSRSASLSKN	74
 : : :	
CKB3	TTTSRVFSSK...DKDPFSFTS.TKTQL.....	66
	. : : . . . : :	
CKB2	TSTSVLMGKQQLHDKESSRSGSISK TNI.....	70
CKB1	NTVSDD..ESDTDSEESDVSGSDGEDTSWISWFCNLRGNEFFCEVDDDYI	122
	. . : : : : : :	
CKB3	...PDV..ESETDSEGSDVSGSEGDDTSWISWFCNLRGNDFFCEVD E DYI	111
	. . : : : : : : :	
CKB2	...SDAVIDSDTDSEESEVSGSDGEDTSWISWFCNLRGNEFFCEVDDDYI	117
CKB1	QDDFNLCGLSSLVPYYEYALDLILDVESSQGEMFTEEQNELIESAAEMLY	172
	: : : . . : : : :	
CKB3	QDDFNLCGLSGQVPYYDYALDLILDVDASNSEMFTDEQH EMVESAAEMLY	161
	: . . : : : :	
CKB2	QDDFNLCGLSHQVPYYDYALDLILDVESSHGEMFTEEQNELIESAAEMLY	167
CKB1	GLIHARYILT SKGLASMLDKYKNYDFGRCP RVYCCGQPCLPVGQS D LPRS	222
	. . : : : . :	
CKB3	GLIHVRYILT TKGMAAMTEKYKNCDFGRCP RVFCCGQSCLPVGQS DI PRS	211
	: . : . : . : : : .	
CKB2	GMIHARFILTSKGLASMLDKYKNYDFGRCP RVYCCGQPCLPVGQS DI PRA	217
CKB1	STVKIYCPKCEDIYYPRSKYQGNIDGAYFGTT FPHLFLMTYGHLKP AKAT	272
	: : . :	
CKB3	STVKIYCPKCEDISYPRSKFQGNIDGAYFGTT FPHLFLMTYGNLK PQ KPT	261
	: : : : .	
CKB2	STVKIYCPKCEDVYYPRSKYQGNIDGAYFGTT FPHLFLMTYGHLKP QK AS	267
CKB1	QNYVQRVFGFKLHKP	287
	. . : :	
CKB3	QSYVPKIFGFKVHKP	276
	. . : :	
CKB2	QSYTORVFGFKLHKP	282



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FIG. 2

SEQ. I.D. No.1

GTCGACCCAC GCGTCCGAGA AGAAAACCCT AGATTTCTCC GTCTCTCTAA TTTCTTTTCT 60
CTCTCAAGCT TCTCAGAAAG TCTGACACTT TCGAGAATCT AATCTCCAAA TTTCTTGTCT 120
TTTTGGAGAA GGAATCGAAT TATGTACAAG GAACGTAGTG GAGGAGGTGG TGGTGGGTCA 180
TCGAGATCAG AGATCCTCGG TGGAGCTATT GATCGGAAAC GAATCAACGA TGCACTCAAT 240
AAGAAACTAG AGAAATCTTC AACTTCCACC ACCACATCTA GGGTTTTCTC TTCTAAAGAC 300
AAAGATCCCT TTTCTTTCAC ATCTACTAAA ACTCAGCTTC CTGATGTGGA ATCGGAAACT 360
GATAGTGAAG GGTCTGATGT GAGTGGATCG GAGGGTGATG ATACGTCGTG GATCTCTTGG 420
TTTTGTAATT TGAGAGGGAA TGATTTCTTC TGTGAAGTCG ATGAAGATTA TATTCAAGAT 480
GATTTCAATC TTTGTGGTTT AAGTGGTCAA GTCCCTTACT ATGATTATGC ACTTGATCTC 540
ATTTTAGATG TTGATGCTTC CAACAGTGAG ATGTTTACTG ATGAACAGCA TGAAATGGTG 600
GAATCAGCTG CTGAGATGCT ATATGGTCTT ATTCATGTTT GTTACATTTT GACTACTAAA 660
GGAATGGCTG CAATGACTGA GAAGTACAAG AACTGTGATT TCGGGAGATG CCCGAGAGTT 720
TTCTGTTGCG GTCAGTCTTG TCTTCCAGTT GGACAATCCG ATATCCCGAG ATCGAGTACT 780
GTGAAGATAT ACTGCCCTAA ATGCGAGGAT ATATCTTACC CGCGATCTAA ATTCCAAGGC 841
AATATTGATG GAGCGTACTT TGGAACCACA TTCCCTCACT TGTTCTTGAT GACTTACGGG 900
AACTTAAAGC CGCAGAAGCC TACTCAAAGC TATGTCCCAA AAATCTTTGG CTTCAGGTA 961
CACAAACCAT GATACTAGTG CTCTGCATTC TCAATGGTGA TACATTTAGT GGCTCTGTAA 1020
TTGCATCCGG ATGAGCAACT GAAACGATAG CTGCGGTGAC TGGAGCATAC ATCAACCATT 1080



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FIG. 3

SEQ. I.D. No.2

Met Tyr Lys Glu Arg Ser Gly Gly Gly Gly Gly Ser Ser Arg Ser Glu Ile Leu Gly 20
Gly Ala Ile Asp Arg Lys Arg Ile Asn Asp Ala Leu Asn Lys Lys Leu Glu Lys Ser Ser 40
Thr Ser Thr Thr Thr Ser Arg Val Phe Ser Ser Lys Asp Lys Asp Pro Phe Ser Phe Thr 60
Ser Thr Lys Thr Gln Leu Pro Asp Val Glu Ser Glu Thr Asp Ser Glu Gly Ser Asp Val 80
Ser Gly Ser Glu Gly Asp Asp Thr Ser Trp Ile Ser Trp Phe Cys Asn Leu Arg Gly Asn 100
Asp Phe Phe Cys Glu Val Asp Glu Asp Tyr Ile Gln Asp Asp Phe Asn Leu Cys Gly Leu 120
Ser Gly Gln Val Pro Tyr Tyr Asp Tyr Ala Leu Asp Leu Ile Leu Asp Val Asp Ala Ser 140
Asn Ser Glu Met Phe Thr Asp Glu Gln His Glu Met Val Glu Ser Ala Ala Glu Met Leu 160
Tyr Gly Leu Ile His Val Arg Tyr Ile Leu Thr Thr Lys Gly Met Ala Ala Met Thr Glu 180
Lys Tyr Lys Asn Cys Asp Phe Gly Arg Cys Pro Arg Val Phe Cys Cys Gly Gln Ser Cys 200
Leu Pro Val Gly Gln Ser Asp Ile Pro Arg Ser Ser Thr Val Lys Ile Tyr Cys Pro Lys 220
Cys Glu Asp Ile Ser Tyr Pro Arg Ser Lys Phe Gln Gly Asn Ile Asp Gly Ala Tyr Phe 240
Gly Thr Thr Phe Pro His Leu Phe Leu Met Thr Tyr Gly Asn Leu Lys Pro Gln Lys Pro 260
Thr Gln Ser Tyr Val Pro Lys Ile Phe Gly Phe Lys Val His Lys Pro 276



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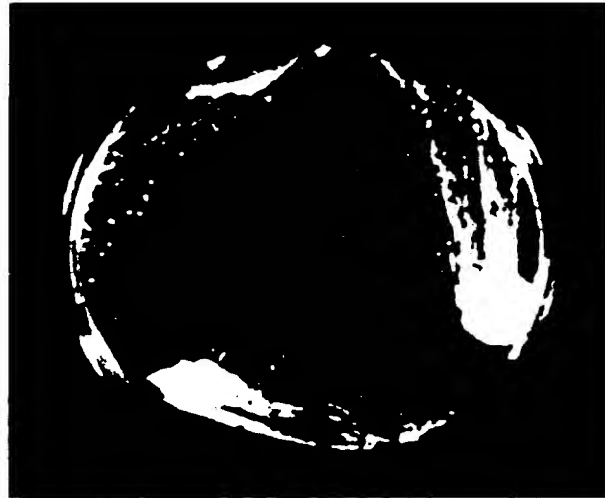


FIG. 4



35.5 °C

pKT10



pJCR14

pKT-CKB3



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FIG. 5A

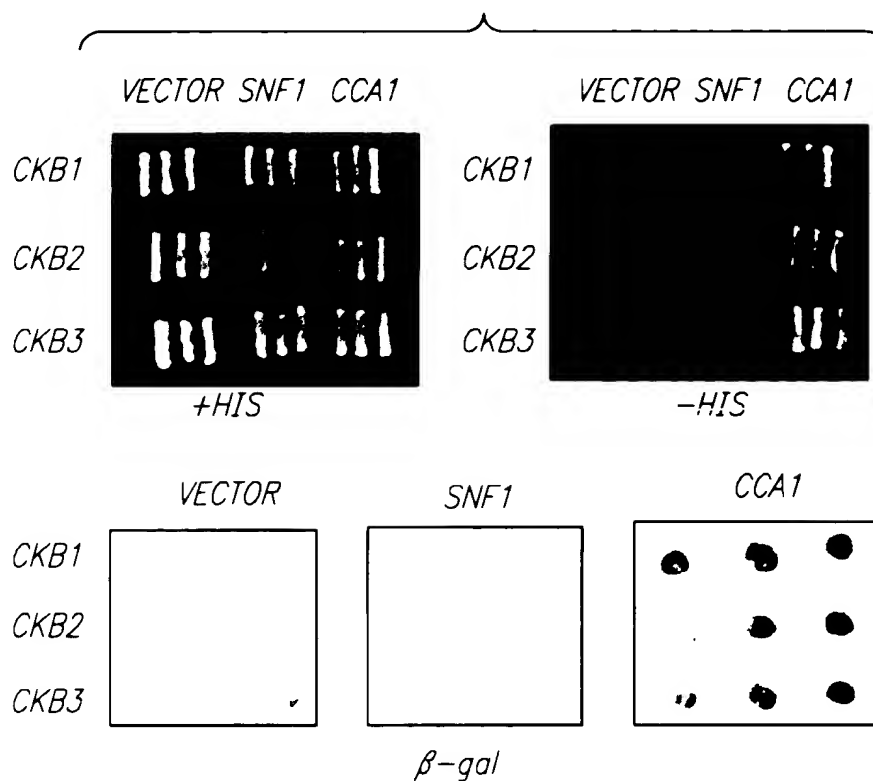
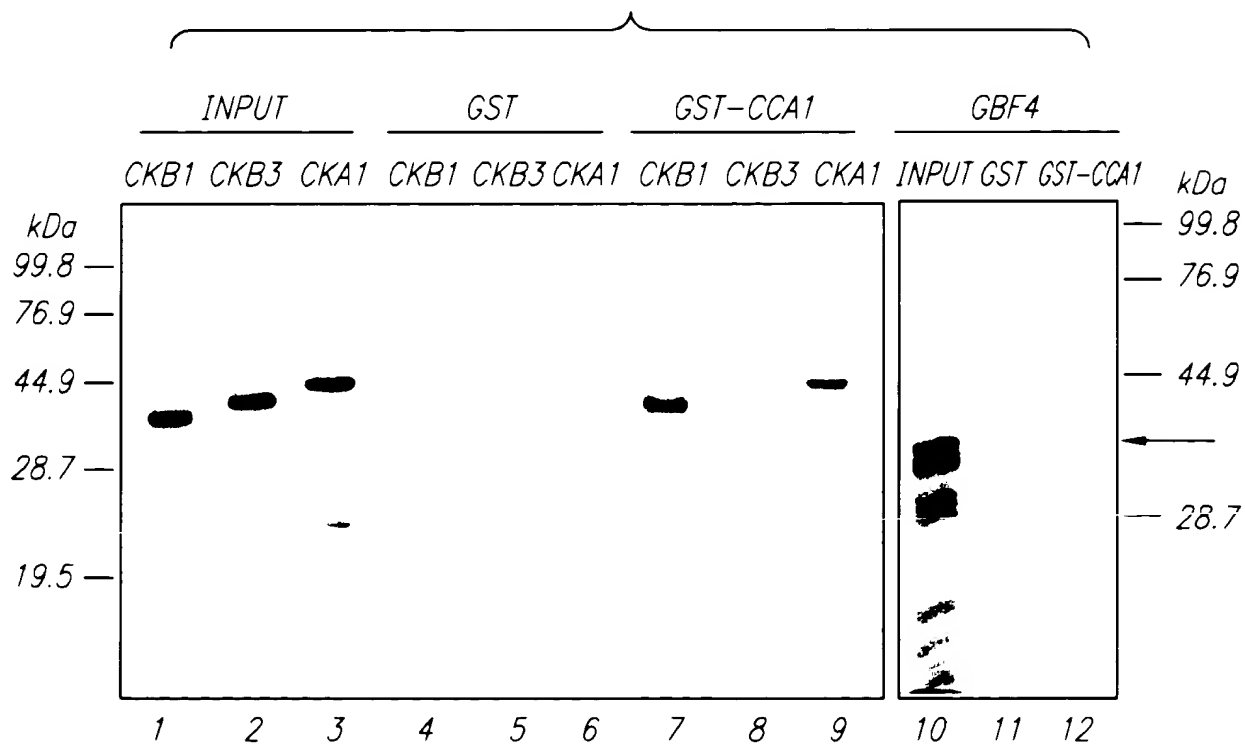


FIG. 5B





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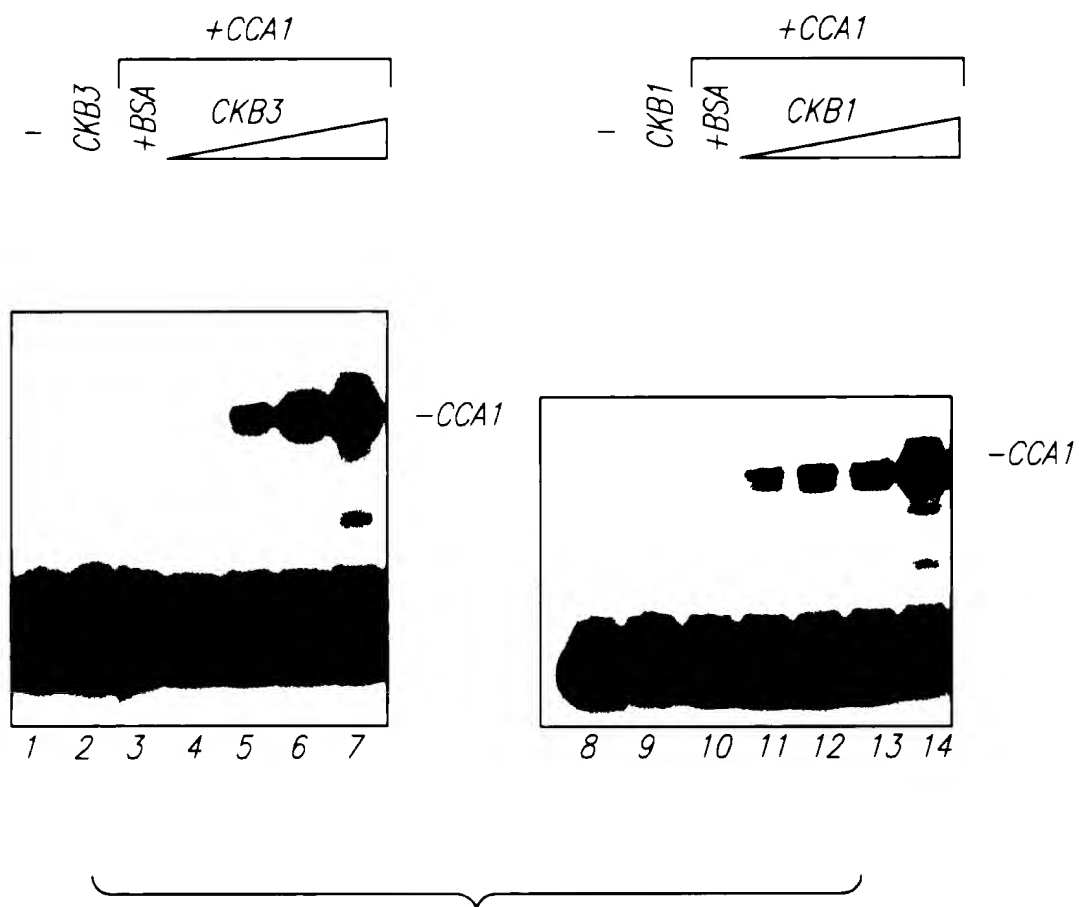


FIG. 6



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FIG. 7B

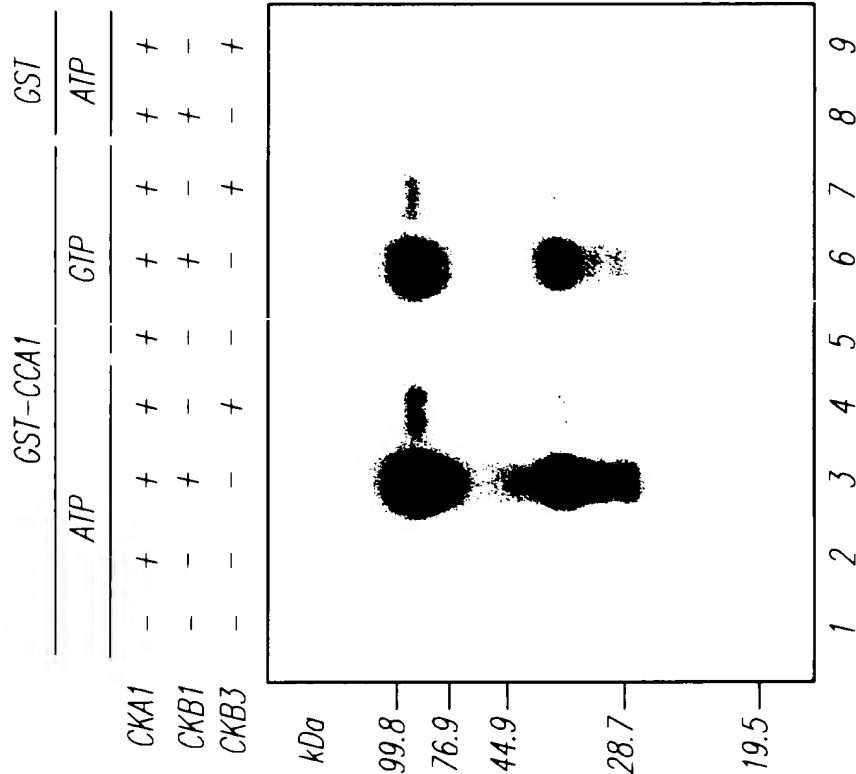
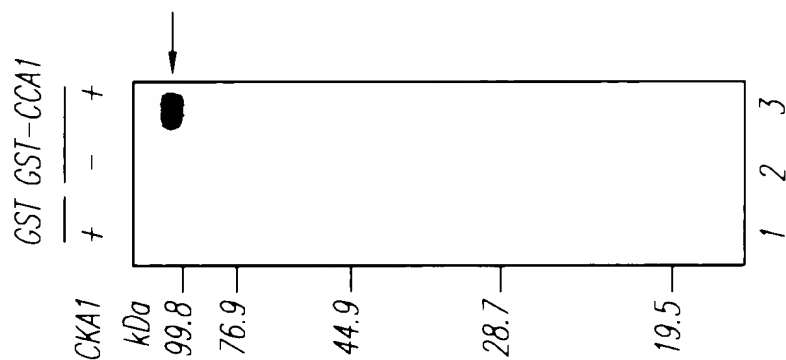
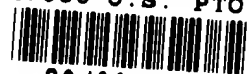


FIG. 7A

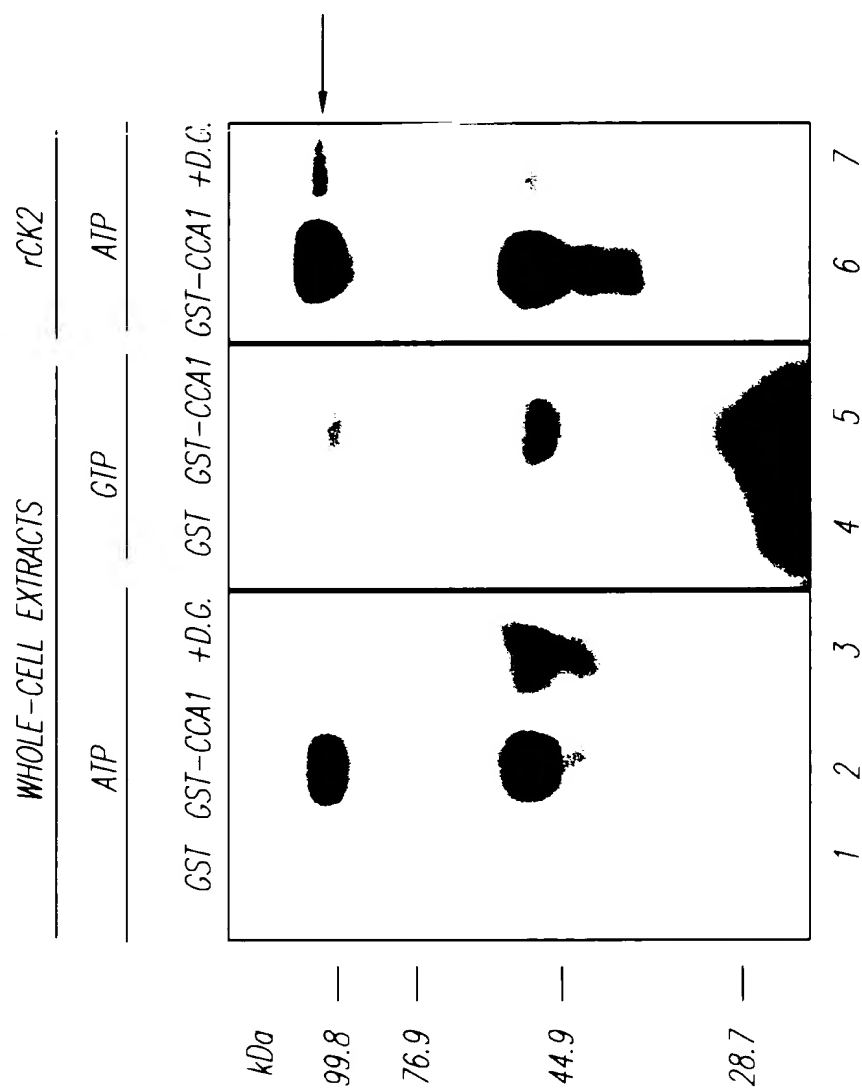




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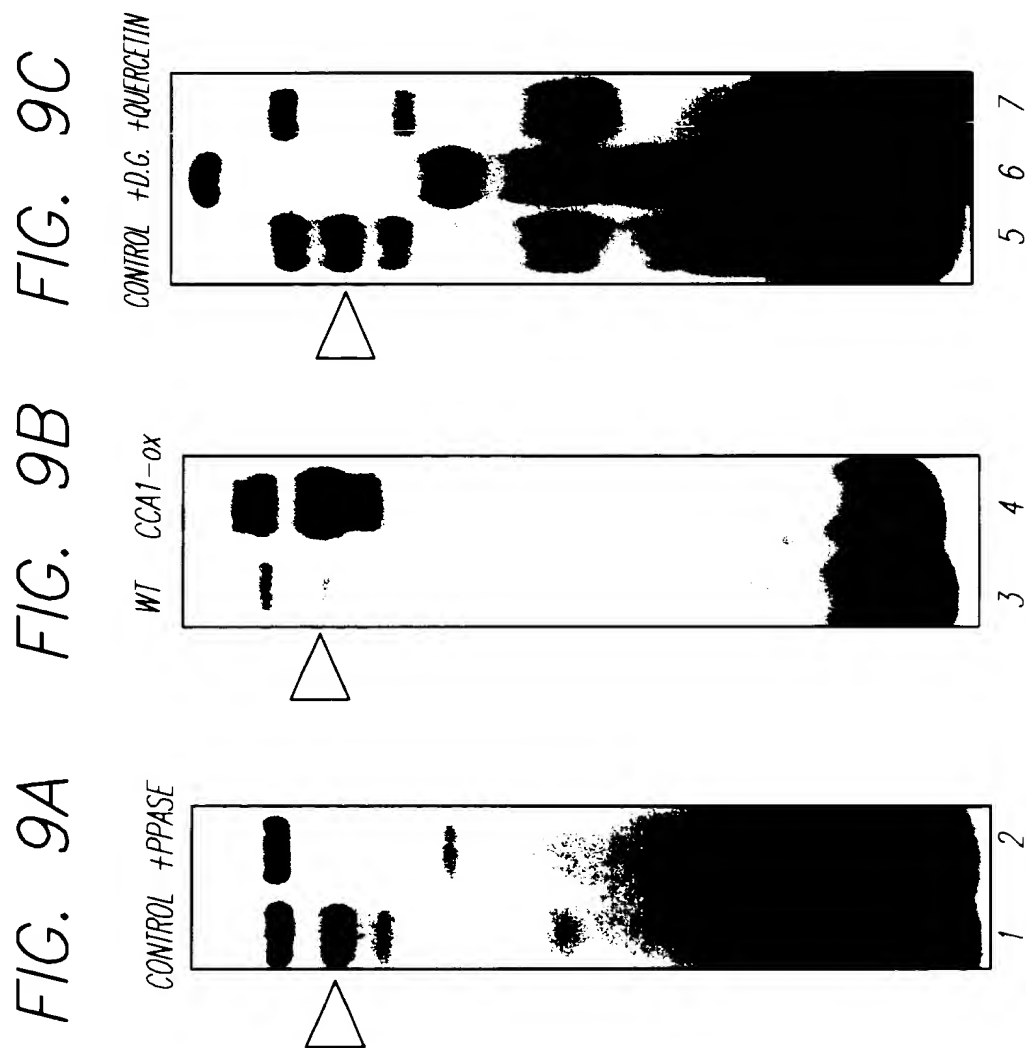
FIG. 8





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FIG. 10A

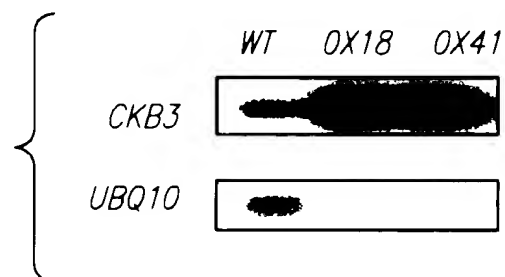


FIG. 10B

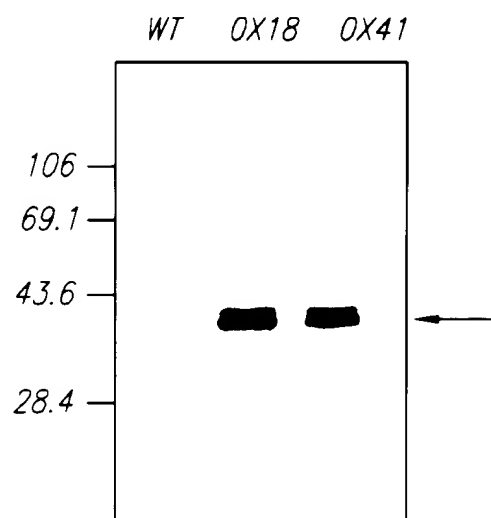
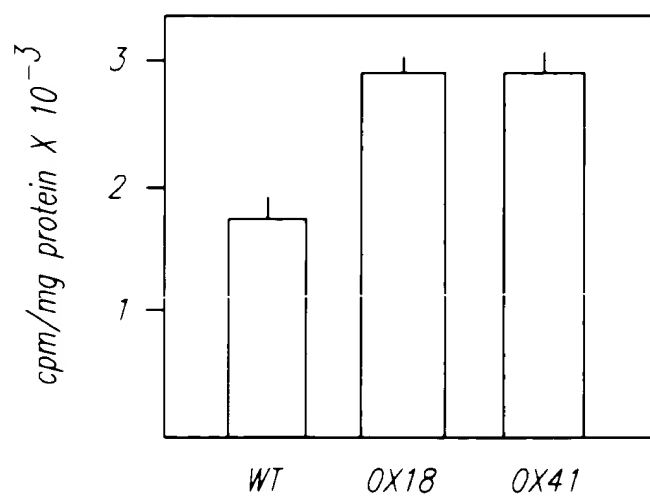


FIG. 10C





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FIG. 11A

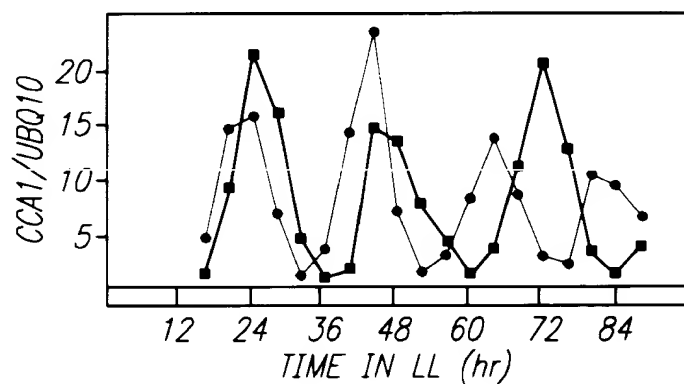
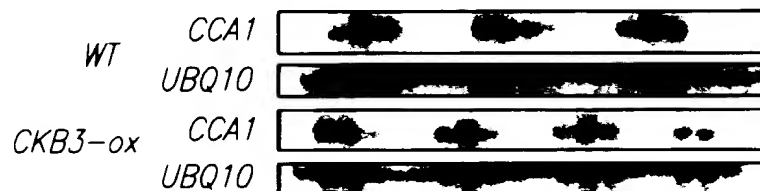


FIG. 11B

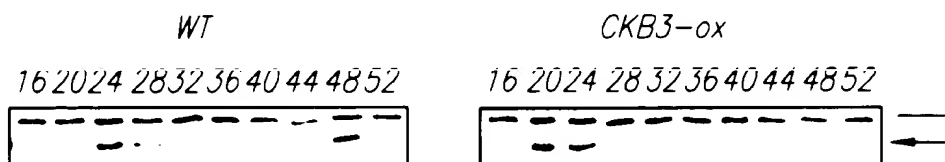
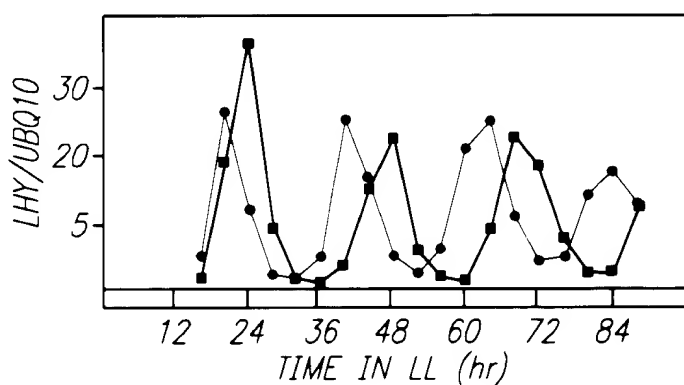
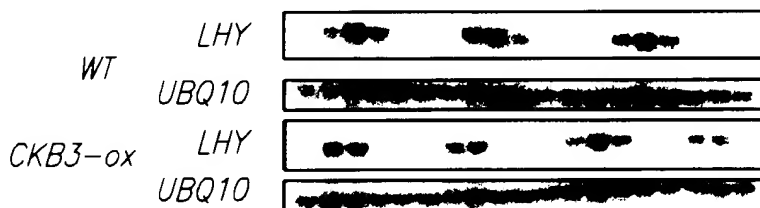


FIG. 11C



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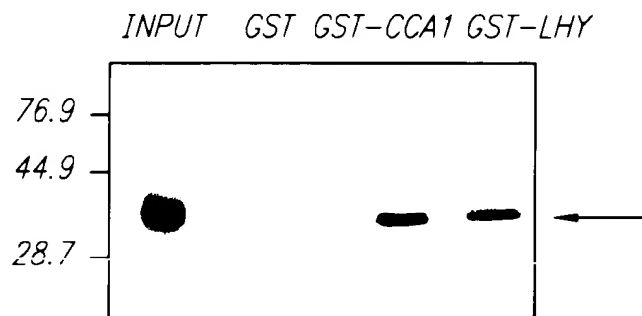


FIG. 12A

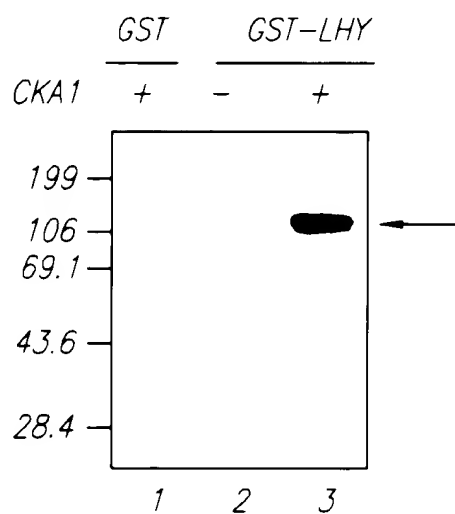


FIG. 12B

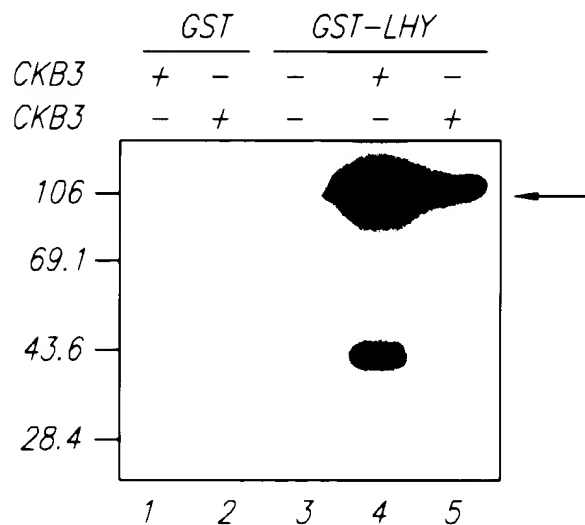


FIG. 12C



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FIG. 13A

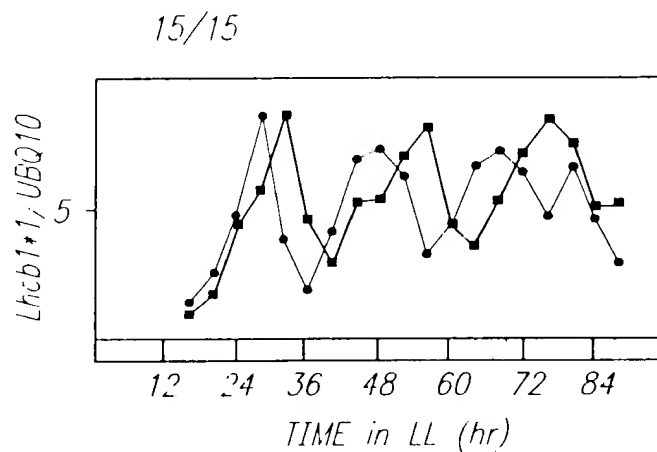


FIG. 13B

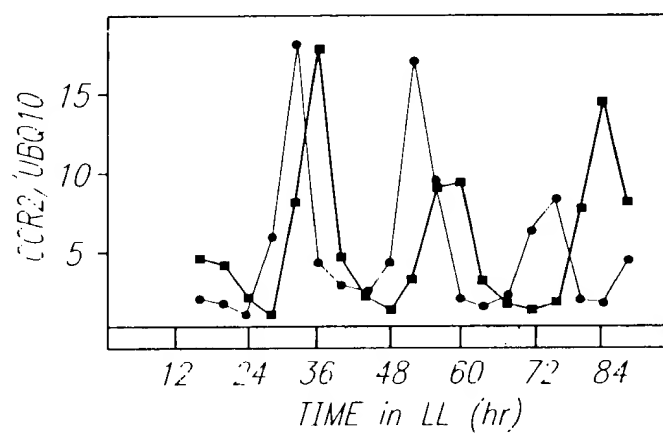


FIG. 13C

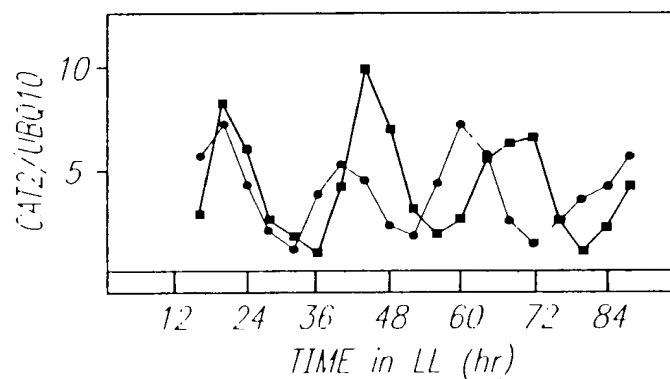


FIG. 13D

